09/770,770

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 NEWS  1          Web Page URLs for STN Seminar Schedule - N. America
 NEWS  2  Sep 17  IMSworld Pharmaceutical Company Directory name change
                  to PHARMASEARCH
 NEWS  3  Oct 09  Korean abstracts now included in Derwent World Patents
                  Index
 NEWS  4  Oct 09  Number of Derwent World Patents Index updates increased
 NEWS  5  Oct 15  Calculated properties now in the REGISTRY/ZREGISTRY File
 NEWS  6  Oct 22  Over 1 million reactions added to CASREACT
 NEWS  7  Oct 22  DGENE GETSIM has been improved
 NEWS  8  Oct 29  AAASD no longer available
 NEWS  9  Nov 19  New Search Capabilities  USPATFULL and USPAT2
 NEWS 10  Nov 19  TOXCENTER(SM) - new toxicology file now available on STN
 NEWS 11  Nov 29  COPPERLIT now available on STN
 NEWS 12  Nov 29  DWPI revisions to NTIS and US Provisional Numbers
 NEWS 13  Nov 30  Files VETU and VETB to have open access
 NEWS 14  Dec 10  WPINDEX/WPIDS/WPIX New and Revised Manual Codes for 2002
 NEWS 15  Dec 10  DGENE BLAST Homology Search
 NEWS 16  Dec 17  WELDASEARCH now available on STN
 NEWS 17  Dec 17  STANDARDS now available on STN
 NEWS 18  Dec 17  New fields for DPCI
 NEWS 19  Dec 19  CAS Roles modified
 NEWS 20  Dec 19  1907-1946 data and page images added to CA and CAplus
 NEWS 21  Jan 25  BLAST(R) searching in REGISTRY available in STN on the Web
 NEWS 22  Jan 25  Searching with the P indicator for Preparations
 NEWS 23  Jan 29  FSTA has been reloaded and moves to weekly updates
 NEWS 24  Feb 01  DKILIT now produced by FIZ Karlsruhe and has a new update
                  frequency

 NEWS EXPRESS  February 1 CURRENT WINDOWS VERSION IS V6.0d,
               CURRENT MACINTOSH VERSION IS V6.0a(ENG) AND V6.0Ja(JP),
               AND CURRENT DISCOVER FILE IS DATED 07 AUGUST 2001
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 NEWS WWW      CAS World Wide Web Site (general information)

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FILE 'HOME' ENTERED AT 15:12:16 ON 05 FEB 2002

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=> s melting temperature#(10a)mismatch##(10a)hybridiz?(10a)plurality(10a)probe#
L1            0 MELTING TEMPERATURE#(10A) MISMATCH##(10A) HYBRIDIZ?(10A) PLURALI
                TY(10A) PROBE#

=> s melting temperature#(10a)mismatch##(10a)hybridiz?(10a)probe#
L2            8 MELTING TEMPERATURE#(10A) MISMATCH##(10A) HYBRIDIZ?(10A) PROBE#

=> s l2 and pluralit###
L3            3 L2 AND PLURALIT###

=> d l3 1-3 bib ab kwic

L3   ANSWER 1 OF 3  USPATFULL
AN     2001:202383  USPATFULL
TI     Rapid-screen cDNA library panels
IN     He, Wei-Wu, Gaithersburg, MD, United States
       Jay, Gilbert, Gaithersburg, MD, United States
PA     Origene Technologies, Inc., Rockville, MD, United States (U.S.
       corporation)
PI     US 6316193          B1   20011113
AI     US 1999-412565           19991005 (9)
RLI    Continuation-in-part of Ser. No. US 1998-166789, filed on 6 Oct 1998
PRAI   US 1998-172222      19981006 (60)
DT     Utility
FS     GRANTED
EXNAM  Primary Examiner: Brusca, John S.; Assistant Examiner: Siu, Stephen
LREP   Millen, White, Zelano, & Branigan, P.C.
CLMN   Number of Claims: 22
ECL    Exemplary Claim: 1
DRWN   No Drawings
LN.CNT 1488
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB     The present invention relates to a arrays of nucleic acid and methods of
       screening these arrays for desired nucleotide sequences. In a preferred
       embodiment of the invention, a desired cDNA clone can be obtained in
       three or less rounds of PCR screening. A master plate containing a
       population of cDNA, distributed in a plurality of wells, is
       screened for a desired clone by PCR. After a master well containing the
       desired cDNA is identified, a second plate containing a cDNA array of
       the master well can then be screened using the same PCR primers. Since
       the second plate contains about 50-fold to 100-fold fewer clones than
       the master plate, an expedient reduction in the number of candidates can
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be achieved in a single PCR step. The invention also relates to a super-master plate containing at least two, preferably more, different populations of cDNA obtainable from different sources of mRNA.

AB . . . obtained in three or less rounds of PCR screening. A master plate containing a population of cDNA, distributed in a **plurality** of wells, is screened for a desired clone by PCR. After a master well containing the desired cDNA is identified, . . .

SUMM The present invention relates to nucleic acid molecules distributed into a **plurality** of containers. In one aspect of the invention, a population of nucleic acid molecules are distributed into multi-well plate containing a **plurality** of receptacles, containers, or depressions ("wells"), such a 24-well, a 96-well, or 384-well plate, etc. In another aspect of the. . .

SUMM . . . the invention is an array of a cDNA population from a desired mRNA source, comprising: a multi-well plate containing a **plurality** of individual wells, each well comprising about 1000-10,000 cDNA clones in aqueous suspension, wherein said cDNA population comprises cDNA of. . .

SUMM . . . sequence; detecting said nucleotide sequence in a second array of a cDNA population, comprising: a second multi-well plate comprising a **plurality** of wells, each well comprising about 10-100 cDNA clones, wherein said second array is an array of said cDNA in. . .

SUMM An object of the invention is an array of a cDNA population, comprising: a multi-well plate comprising a **plurality** of wells, each well comprising about 10-100 cDNA clones in aqueous suspension, and said cDNA population is an array of. . .

SUMM An object of the present invention is an array of a cDNA population, comprising a **plurality** of plates, each plate comprising a **plurality** of wells, each well comprising about 10-100 cDNA clones in aqueous suspension, wherein said cDNA population comprises cDNA of a predetermined size and each well contains a different content cDNAs; and said **plurality** of plates is representative of substantially all mRNA of a predetermined size of said source. Optionally, wherein each well comprises. . .

SUMM . . . in a single multi-well plate, each population prepared from a different source of mRNA, comprising: a multi-well plate containing a **plurality** of individual wells, each well comprising about 30,000-100,000 cDNA clones in aqueous suspension, wherein each different cDNA population comprises mRNA. . .

SUMM . . . in a single multi-well plate, each population obtainable from a different source of mRNA, comprising: a multi-well plate comprising a **plurality** of individual wells, wherein a subset of individual wells comprises a cDNA population in an aqueous suspension which is representative. . .

SUMM . . . of an aqueous suspension of a cDNA population obtainable from a desired mRNA source, comprising: a multi-well plate containing a **plurality** of individual wells, each individual well containing an aqueous suspension of a different content of said cDNA population, wherein said. . .

SUMM . . . then subdivided into pools which can be distributed into a series of receptacles, such as a multi-well plate containing a **plurality** of individual wells, e.g., a 24-well, 96-well, 384-well, etc., plate. Alternatively, the cDNA can be isolated from the vector and then arrayed into the multi-well plate. The term "plate" as used herein means, e.g., a single piece comprising a **plurality** of receptacles into which nucleic acid can be contained. A plate can be manufactured as a single piece or assembled. . .

SUMM . . . of an aqueous suspension of a cDNA population obtainable from a desired mRNA source, comprising: a multi-well plate containing a **plurality** of individual wells, each individual well containing an aqueous suspension of a different content of said cDNA population, wherein said. . .

SUMM . . . of the invention is a cDNA population from a desired mRNA source arrayed in a single multi-well plate containing a

plurality of individual wells. Each well is preferably different in its content of cDNA. Generally, when a cDNA population is prepared. . .

SUMM . . . to ensure that probe and target hybridize. Mismatches can be allowed for by lowering the temperature still further. A 1% **mismatch** between the target and **probe** sequences lowers the **melting temperature** by 1.degree.-1.5.degree. C., so **hybridization** and washing at lower temperatures can be used to allow for mismatch. The greater the degree of mismatch allowed, the. . .

SUMM . . . nucleic acid amplification techniques (e.g., differential display or mismatch repair), where each PCR round is performed on plate comprising a **plurality** of wells. In general, a small number of plates, e.g., one, two, three, or four, containing an entire first population. . .

SUMM . . . in a single multi-well plate, each population prepared from a different source of mRNA, comprising: a multi-well plate containing a **plurality** of individual wells, each well comprising about 1,000-70,000 about 20,000-120,000, about 30,000-100,000, about 50,000-80,000, about 50,000-70,000 etc, cDNA clones in. . .

SUMM . . . in a single multi-well plate, each population obtainable from a different source of mRNA, comprising: a multi-well plate comprising a **plurality** of individual wells, wherein a subset of individual wells comprises a cDNA population in an aqueous suspension which is representative. . .

SUMM pooling samples from a **plurality** of wells of a multi-well plate to form a **plurality** of pools, said multi-well plate comprising a **plurality** of individual wells in rows and columns, each well comprising at least one representative of an independent DNA clone, and. . . one primer is specific for a gene present in at least one DNA clone; detecting amplified DNA product from a **plurality** of said pools; identifying the presence of a full-length DNA clone in a pool which is representative of said gene, or the presence of multiple different DNA clones in a **plurality** of pools which are representative of multiple different transcripts originating from said gene, etc.

SUMM In preferred embodiments, samples are pooled from a **plurality** of wells, e.g., at least two. In the most preferred embodiment, samples are pooled from all the wells in a. . .

CLM What is claimed is:

1. An array of a cDNA population from a desired mRNA source, comprising: a multi-well plate containing a **plurality** of individual wells, each well comprising about 1000-10,000 cDNA clones in aqueous suspension, wherein said cDNA population comprises full-length cDNA. . .

. . . in a single multi-well plate, each population obtainable from a different source of mRNA, comprising: a multi-well plate comprising a **plurality** of individual wells, wherein a subset of individual wells comprises a cDNA population in an aqueous suspension which is representative. . .

. . . of a cDNA population comprising normalized full-length cDNAs from at least one mRNA source, comprising: a multi-well plate containing a **plurality** of individual wells, each well comprising cDNAs in an aqueous suspension, wherein said cDNAs comprise normalized full-length cDNAs of a. . .

17. An array of an aqueous suspension in a single multi-well plate of normalized cDNA population from a **plurality** of different sources of mRNA, comprising; a multi-well plate containing a **plurality** of individual wells, each well comprising normalized full-length cDNAs of a preselected size, at least two wells in said plate. . . of said normalized cDNA population in all the wells of said plate is representative of substantially all mRNA from said **plurality** of sources.

L3 ANSWER 2 OF 3 USPATFULL
AN 2001:139278 USPATFULL
TI Rapid-screen cDNA library panels
IN He, Wei-Wu, Gaithersburg, MD, United States
Jay, Gilbert, Gaithersburg, MD, United States
PI US 2001016320 A1 20010823
AI US 2001-764317 A1 20010119 (9)
RLI Division of Ser. No. US 1999-412565, filed on 5 Oct 1999, PENDING
Continuation-in-part of Ser. No. US 1998-166789, filed on 6 Oct 1998, ABANDONED
DT Utility
FS APPLICATION
LREP MILLEN, WHITE, ZELANO & BRANIGAN, P.C., Arlington Courthouse Plaza I, Suite 1400, 2200 Clarendon Boulevard, Arlington, VA, 22201
CLMN Number of Claims: 18
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 1507
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to a arrays of nucleic acid and methods of screening these arrays for desired nucleotide sequences. In a preferred embodiment of the invention, a desired cDNA clone can be obtained in three or less rounds of PCR screening. A master plate containing a population of cDNA, distributed in a **plurality** of wells, is screened for a desired clone by PCR. After a master well containing the desired cDNA is identified, a second plate containing a cDNA array of the master well can then be screened using the same PCR primers. Since the second plate contains about 50-fold to 100-fold fewer clones than the master plate, an expedient reduction in the number of candidates can be achieved in a single PCR step. The invention also relates to a super-master plate containing at least two, preferably more, different populations of cDNA obtainable from different sources of mRNA.
AB . . . obtained in three or less rounds of PCR screening. A master plate containing a population of cDNA, distributed in a **plurality** of wells, is screened for a desired clone by PCR. After a master well containing the desired cDNA is identified,. . .
SUMM [0003] The present invention relates to nucleic acid molecules distributed into a **plurality** of containers. In one aspect of the invention, a population of nucleic acid molecules are distributed into multi-well plate containing a **plurality** of receptacles, containers, or depressions ("wells"), such a 24-well, a 96-well, or 384-well plate, etc. In another aspect of the. . .
SUMM . . . the invention is an array of a cDNA population from a desired MRNA source, comprising: a multi-well plate containing a **plurality** of individual wells, each well comprising about 1000-10,000 cDNA clones in aqueous suspension, wherein said cDNA population comprises cDNA of. . .
SUMM . . . sequence; detecting said nucleotide sequence in a second array of a cDNA population, comprising: a second multi-well plate comprising a **plurality** of wells, each well comprising about 10-100 cDNA clones, wherein said second array is an array of said cDNA in. . .
SUMM [0006] An object of the invention is an array of a cDNA population, comprising: a multi-well plate comprising a **plurality** of wells, each well comprising about 10-100 cDNA clones in aqueous suspension, and said cDNA population is an array of. . .
SUMM [0007] An object of the present invention is an array of a cDNA population, comprising a **plurality** of plates, each plate comprising a **plurality** of wells, each well comprising about 10-100 cDNA clones in aqueous suspension, wherein said cDNA population comprises cDNA of a predetermined size and each well contains a different content cDNAs; and said **plurality** of plates is representative of substantially all mRNA of a predetermined size of said source. Optionally, wherein each well comprises. . .

SUMM . . . in a single multi-well plate, each population prepared from a different source of mRNA, comprising: a multi-well plate containing a **plurality** of individual wells, each well comprising about 30,000-100,000 cDNA clones in aqueous suspension, wherein each different cDNA population comprises MRNA. . .

SUMM . . . in a single multi-well plate, each population obtainable from a different source of mRNA, comprising: a multi-well plate comprising a **plurality** of individual wells, wherein a subset of individual wells comprises a cDNA population in an aqueous suspension which is representative. . .

SUMM . . . of an aqueous suspension of a cDNA population obtainable from a desired mRNA source, comprising: a multi-well plate containing a **plurality** of individual wells, each individual well containing an aqueous suspension of a different content of said cDNA population, wherein said. . .

SUMM . . . then subdivided into pools which can be distributed into a series of receptacles, such as a multi-well plate containing a **plurality** of individual wells, e.g., a 24-well, 96-well, 384-well, etc., plate. Alternatively, the cDNA can be isolated from the vector and then arrayed into the multi-well plate. The term "plate" as used herein means, e.g., a single piece comprising a **plurality** of receptacles into which nucleic acid can be contained. A plate can be manufactured as a single piece or assembled. . .

SUMM . . . of an aqueous suspension of a cDNA population obtainable from a desired MRNA source, comprising: a multi-well plate containing a **plurality** of individual wells, each individual well containing an aqueous suspension of a different content of said cDNA population, wherein said. . .

SUMM . . . of the invention is a CDNA population from a desired mRNA source arrayed in a single multi-well plate containing a **plurality** of individual wells. Each well is preferably different in its content of cDNA. Generally, when a CDNA population is prepared. . .

SUMM . . . to ensure that probe and target hybridize. Mismatches can be allowed for by lowering the temperature still further. A 1% **mismatch** between the target and **probe** sequences lowers the **melting temperature** by 1.degree.-1.5.degree. C., so **hybridization** and washing at lower temperatures can be used to allow for mismatch. The greater the degree of mismatch allowed, the. . .

SUMM . . . nucleic acid amplification techniques (e.g., differential display or mismatch repair), where each PCR round is performed on plate comprising a **plurality** of wells. In general, a small number of plates, e.g., one, two, three, or four, containing an entire first population. . .

SUMM . . . in a single multi-well plate, each population prepared from a different source of MRNA, comprising: a multi-well plate containing a **plurality** of individual wells, each well comprising about 1,000-70,000 about 20,000-120,000, about 30,000-100,000, about 50,000-80,000, about 50,000-70,000 etc, cDNA clones in. . .

SUMM . . . in a single multi-well plate, each population obtainable from a different source of mRNA, comprising: a multi-well plate comprising a **plurality** of individual wells, wherein a subset of individual wells comprises a cDNA population in an aqueous suspension which is representative. . .

SUMM [0040] pooling samples from a **plurality** of wells of a multi-well plate to form a **plurality** of pools, said multi-well plate comprising a **plurality** of individual wells in rows and columns, each well comprising at least one representative of an independent DNA clone, and. . . one primer is specific for a gene present in at least one DNA clone; detecting amplified DNA product from a **plurality** of said pools; identifying the presence of a full-length DNA clone in a pool which is representative of said gene, or the presence of multiple different DNA clones in a **plurality**

of pools which are representative of multiple different transcripts originating from said gene, etc.

SUMM [0042] In preferred embodiments, samples are pooled from a **plurality** of wells, e.g., at least two. In the most preferred embodiment, samples are pooled from all the wells in a. . .

CLM What is claimed is:

. . . DNA clones or multiple different DNA clones representing multiple transcripts originating from the same gene, comprising: pooling samples from a **plurality** of wells of a multi-well plate to form a **plurality** of pools, said multi-well plate comprising a **plurality** of individual wells in rows and columns, each well comprising at least one representative of 4,000-12,000 independent DNA clones, and. . . one primer is specific for a gene present in at least one DNA clone, detecting amplified DNA product from a **plurality** of said pools, and identifying the size of a DNA clone in a pool which is representative of said gene, or the presence of multiple different DNA clones in a **plurality** of pools which are representative of multiple different transcripts originating from said gene.

2. A method of claim 1, wherein said pools are formed by pooling samples from a **plurality** of wells in a column and/or a row.

. . . wells or columns which contain DNA product having the same size, whereby the presence of same-sized DNA product in a **plurality** of pools indicates the presence of a DNA clone representing a full-length or a specific transcript of said gene.

. . . wells or columns which contain DNA product having the same size, whereby the presence of same-sized DNA product in a **plurality** of pools indicates the presence of a DNA clone representing a specific transcript of said gene.

11. An array of a cDNA population from a desired MRNA source, comprising: a multi-well plate containing a **plurality** of individual wells, each well comprising about 1000-10,000 cDNA clones in aqueous suspension, wherein said cDNA population comprises cDNA of. . .

. . . in a single multi-well plate, each population obtainable from a different source of mRNA, comprising: a multi-well plate comprising a **plurality** of individual wells, wherein a subset of individual wells comprises a cDNA population in an aqueous suspension which is representative. . .

L3 ANSWER 3 OF 3 USPATFULL
AN 97:117888 USPATFULL
TI Nucleotide sequences and methods for detection of Serpulina hyodysenteriae
IN Duhamel, Gerald E., Lincoln, NE, United States
Elder, Robert, Lincoln, NE, United States
PA Board of Regents of the University of Nebraska, NE, United States (U.S. corporation)
PI US 5698394 19971216
AI US 1994-252492 19940601 (8)
DT Utility
FS Granted
EXNAM Primary Examiner: Elliott, George C.; Assistant Examiner: Fredman, Jeffrey
LREP Suiter & Associates PC
CLMN Number of Claims: 22
ECL Exemplary Claim: 1
DRWN 6 Drawing Figure(s); 6 Drawing Page(s)
LN.CNT 2379
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The invention provides a method for detecting the presence of Serpulina hyodysenteriae in a biological sample, an oligonucleotide primer and an S. hyodysenteriae-specific oligonucleotide probe useful in that method, and an article of manufacture that contains the primers and/or probe. Also provided are an about 2.3-kb DNA fragment derived from genomic DNA of S. hyodysenteriae and encoding for an about 56 kDa polypeptide, a recombinant expression vector containing the DNA fragment, the 56 kDa polypeptide and a monoclonal antibody reactive with the peptide, and a method of assaying for antibodies reactive with the 56 kDa peptide.

DETD . . . about 20 to 2300 nucleotides can have up to about 30% mismatches and still hybridize to the target sequence. Mismatched **probes** can still hybridize to the target sequence if conditions of **hybridization** are modified to account for the **mismatch**, as, for example, by decreasing **melting temperature** by about 1.0 to 1.5.degree. C. for every 1% of mismatch. Because a target DNA sequence has been cloned and. . .

CLM What is claimed is:
13. The method according to claim 2, further comprising placing amplification products from each biological sample of a **plurality** of biological samples into a different well of a multiwell plate.

=> d l2 1-8 bib ab

L2 ANSWER 1 OF 8 USPATFULL
AN 2001:202383 USPATFULL
TI Rapid-screen cDNA library panels
IN He, Wei-Wu, Gaithersburg, MD, United States
Jay, Gilbert, Gaithersburg, MD, United States
PA Origene Technologies, Inc., Rockville, MD, United States (U.S. corporation)
PI US 6316193 B1 20011113
AI US 1999-412565 19991005 (9)
RLI Continuation-in-part of Ser. No. US 1998-166789, filed on 6 Oct 1998
PRAI US 1998-172222 19981006 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Brusca, John S.; Assistant Examiner: Siu, Stephen
LREP Millen, White, Zelano, & Branigan, P.C.
CLMN Number of Claims: 22
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 1488
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to a arrays of nucleic acid and methods of screening these arrays for desired nucleotide sequences. In a preferred embodiment of the invention, a desired cDNA clone can be obtained in three or less rounds of PCR screening. A master plate containing a population of cDNA, distributed in a plurality of wells, is screened for a desired clone by PCR. After a master well containing the desired cDNA is identified, a second plate containing a cDNA array of the master well can then be screened using the same PCR primers. Since the second plate contains about 50-fold to 100-fold fewer clones than the master plate, an expedient reduction in the number of candidates can be achieved in a single PCR step. The invention also relates to a super-master plate containing at least two, preferably more, different populations of cDNA obtainable from different sources of mRNA.

L2 ANSWER 2 OF 8 USPATFULL
AN 2001:139278 USPATFULL
TI Rapid-screen cDNA library panels
IN He, Wei-Wu, Gaithersburg, MD, United States

Jay, Gilbert, Gaithersburg, MD, United States
PI US 2001016320 A1 20010823
AI US 2001-764317 A1 20010119 (9)
RLI Division of Ser. No. US 1999-412565, filed on 5 Oct 1999, PENDING
Continuation-in-part of Ser. No. US 1998-166789, filed on 6 Oct 1998, ABANDONED
DT Utility
FS APPLICATION
LREP MILLEN, WHITE, ZELANO & BRANIGAN, P.C., Arlington Courthouse Plaza I, Suite 1400, 2200 Clarendon Boulevard, Arlington, VA, 22201
CLMN Number of Claims: 18
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 1507
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to a arrays of nucleic acid and methods of screening these arrays for desired nucleotide sequences. In a preferred embodiment of the invention, a desired cDNA clone can be obtained in three or less rounds of PCR screening. A master plate containing a population of cDNA, distributed in a plurality of wells, is screened for a desired clone by PCR. After a master well containing the desired cDNA is identified, a second plate containing a cDNA array of the master well can then be screened using the same PCR primers. Since the second plate contains about 50-fold to 100-fold fewer clones than the master plate, an expedient reduction in the number of candidates can be achieved in a single PCR step. The invention also relates to a super-master plate containing at least two, preferably more, different populations of cDNA obtainable from different sources of mRNA.

L2 ANSWER 3 OF 8 USPATFULL
AN 2000:162099 USPATFULL
TI Computer logic for fluorescence genotyping at multiple allelic sites
IN Livak, Kenneth J., San Jose, CA, United States
Goodsaid, Federico, San Jose, CA, United States
PA PE Applied Biosystems, a division of Perkin-Elmer, Foster City, CA, United States (U.S. corporation)
PI US 6154707 20001128
AI US 1999-324709 19990603 (9)
RLI Division of Ser. No. US 1998-18595, filed on 4 Feb 1998
DT Utility
FS Granted
EXNAM Primary Examiner: Fredman, Jeffrey
LREP Weitz, David J.Wilson Sonsini Goodrich & Rosati
CLMN Number of Claims: 1
ECL Exemplary Claim: 1
DRWN 25 Drawing Figure(s); 17 Drawing Page(s)
LN.CNT 1733
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A method is provided for genotyping a target sequence at at least two allelic sites by a 5' nuclease amplification reaction. In one embodiment, the method includes performing a nucleic acid amplification on a target sequence having at least two different allelic sites using a nucleic acid polymerase having 5'.fwdarw.3' nuclease activity and a primer capable of hybridizing to the target sequence in the presence of two or more sets of allelic oligonucleotide probes wherein:

each set of allelic oligonucleotide probes is for detecting a different allelic site of the target sequence,

each set of allelic oligonucleotide probes includes two or more probes which are complementary to different allelic variants at the allelic site being detected by the set of probes, the allelic site being 5' relative to a sequence to which the primer hybridizes to the target sequence, and

at least all but one of the allelic oligonucleotide probes include a different fluorescer than the other probes and a quencher positioned on the probe to quench the fluorescence of the fluorescer;

detecting a fluorescence spectrum of the amplification;

calculating a fluorescence contribution of each fluorescer to the fluorescence spectrum; and

determining a presence or absence of the different allelic variants at the two or more different allelic sites based on the fluorescence contribution of each fluorescer to the combined fluorescence spectrum.

L2 ANSWER 4 OF 8 USPATFULL
AN 2000:67434 USPATFULL
TI Nucleotide sequences and methods for detection of Serpulina hyodysenteriae
IN Duhamel, Gerald E., Lincoln, NE, United States
Elder, Robert, Lincoln, NE, United States
PA Board of Regents University of Nebraska, Lincoln, NE, United States (U.S. corporation)
PI US 6068843 20000530
AI US 1997-942761 19971002 (8)
RLI Division of Ser. No. US 1996-727126, filed on 8 Oct 1996, now patented, Pat. No. US 5869630 which is a division of Ser. No. US 1994-252492, filed on 1 Jun 1994, now patented, Pat. No. US 5698394
DT Utility
FS Granted
EXNAM Primary Examiner: Housel, James C.; Assistant Examiner: Hines, Ja-Na Amira
LREP Suiter & Associates PC
CLMN Number of Claims: 2
ECL Exemplary Claim: 1
DRWN 6 Drawing Figure(s); 6 Drawing Page(s)
LN.CNT 2284
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention provides a method for detecting the presence of Serpulina hyodysenteriae in a biological sample, an oligonucleotide primer and an S. hyodysenteriae-specific oligonucleotide probe useful in that method, and an article of manufacture that contains the primers and/or probe. Also provided are an about 2.3-kb DNA fragment derived from genomic DNA of S. hyodysenteriae and encoding for an about 56 kDa polypeptide, a recombinant expression vector containing the DNA fragment, the 56 kDa polypeptide and a monoclonal antibody reactive with the peptide, and a method of assaying for antibodies reactive with the 56 kDa peptide.

L2 ANSWER 5 OF 8 USPATFULL
AN 1999:121136 USPATFULL
TI Determination of a genotype of an amplification product at multiple allelic sites
IN Livak, Kenneth J., San Jose, CA, United States
Goodsaid, Federico, San Jose, CA, United States
PA The Perkin-Elmer Corporation, Foster City, CA, United States (U.S. corporation)
PI US 5962233 19991005
AI US 1998-18595 19980204 (9)
DT Utility
FS Granted
EXNAM Primary Examiner: Fredman, Jeffrey
LREP Weitz, David J.Wilson Sonsini Goodrich & Rosati
CLMN Number of Claims: 56
ECL Exemplary Claim: 1
DRWN 22 Drawing Figure(s); 17 Drawing Page(s)

LN.CNT 1973
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A method is provided for genotyping a target sequence at at least two allelic sites by a 5' nuclease amplification reaction. In one embodiment, the method includes performing a nucleic acid amplification on a target sequence having at least two different allelic sites using a nucleic acid polymerase having 5'.fwdarw.3' nuclease activity and a primer capable of hybridizing to the target sequence in the presence of two or more sets of allelic oligonucleotide probes wherein:

each set of allelic oligonucleotide probes is for detecting a different allelic site of the target sequence,

each set of allelic oligonucleotide probes includes two or more probes which are complementary to different allelic variants at the allelic site being detected by the set of probes, the allelic site being 5' relative to a sequence to which the primer hybridizes to the target sequence, and

at least all but one of the allelic oligonucleotide probes include a different fluorescer than the other probes and a quencher positioned on the probe to quench the fluorescence of the fluorescer;

detecting a fluorescence spectrum of the amplification;

calculating a fluorescence contribution of each fluorescer to the fluorescence spectrum; and

determining a presence or absence of the different allelic variants at the two or more different allelic sites based on the fluorescence contribution of each fluorescer to the combined fluorescence spectrum.

L2 ANSWER 6 OF 8 USPATFULL
AN 1999:19291 USPATFULL
TI Nucleotide sequences for detection of serpulina hyodysenteriae
IN Duhamel, Gerald E., Lincoln, NE, United States
Elder, Robert, Lincoln, NE, United States
PA Board of Regents, University of Nebraska Lincoln, Lincoln, NE, United States (U.S. corporation)
PI US 5869630 19990209
AI US 1996-727126 19961008 (8)
RLI Division of Ser. No. US 1994-252492, filed on 1 Jun 1994
DT Utility
FS Granted
EXNAM Primary Examiner: Zitomer, Stephanie W.; Assistant Examiner: Fredman, Jeffrey
LREP Suiter & Associates PC
CLMN Number of Claims: 17
ECL Exemplary Claim: 1
DRWN 7 Drawing Figure(s); 6 Drawing Page(s)
LN.CNT 2256
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention provides a method for detecting the presence of Serpulina hyodysenteriae in a biological sample, an oligonucleotide primer and an S. hyodysenteriae-specific oligonucleotide probe useful in that method, and an article of manufacture that contains the primers and/or probe. Also provided are an about 2.3-kb DNA fragment derived from genomic DNA of S. hyodysenteriae and encoding for an about 56 kDa polypeptide, a recombinant expression vector containing the DNA fragment, the 56 kDa polypeptide and a monoclonal antibody reactive with the peptide, and a method of assaying for antibodies reactive with the 56 kDa peptide.

L2 ANSWER 7 OF 8 USPATFULL
AN 1998:82535 USPATFULL

TI Artificial mismatch hybridization
IN Guo, Zhen, Madison, WI, United States
Smith, Lloyd M., Madison, WI, United States
PA Wisconsin Alumni Research Foundation, Madison, WI, United States (U.S. corporation)
PI US 5780233 19980714
AI US 1996-659605 19960606 (8)
DT Utility
FS Granted
EXNAM Primary Examiner: Zitomer, Stephanie W.; Assistant Examiner: Shoemaker, Debra
LREP Quarles & Brady
CLMN Number of Claims: 5
ECL Exemplary Claim: 1
DRWN 8 Drawing Figure(s); 8 Drawing Page(s)
LN.CNT 888
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB An improved nucleic acid hybridization process is provided which employs a modified oligonucleotide and improves the ability to discriminate a control nucleic acid target from a variant nucleic acid target containing a sequence variation. The modified probe contains at least one artificial mismatch relative to the control nucleic acid target in addition to any mismatch(es) arising from the sequence variation. The invention has direct and advantageous application to numerous existing hybridization methods, including, applications that employ, for example, the Polymerase Chain Reaction, allele-specific nucleic acid sequencing methods, and diagnostic hybridization methods.

L2 ANSWER 8 OF 8 USPATFULL
AN 97:117888 USPATFULL
TI Nucleotide sequences and methods for detection of Serpulina hyodysenteriae
IN Duhamel, Gerald E., Lincoln, NE, United States
Elder, Robert, Lincoln, NE, United States
PA Board of Regents of the University of Nebraska, NE, United States (U.S. corporation)
PI US 5698394 19971216
AI US 1994-252492 19940601 (8)
DT Utility
FS Granted
EXNAM Primary Examiner: Elliott, George C.; Assistant Examiner: Fredman, Jeffrey
LREP Suiter & Associates PC
CLMN Number of Claims: 22
ECL Exemplary Claim: 1
DRWN 6 Drawing Figure(s); 6 Drawing Page(s)
LN.CNT 2379
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention provides a method for detecting the presence of Serpulina hyodysenteriae in a biological sample, an oligonucleotide primer and an S. hyodysenteriae-specific oligonucleotide probe useful in that method, and an article of manufacture that contains the primers and/or probe. Also provided are an about 2.3-kb DNA fragment derived from genomic DNA of S. hyodysenteriae and encoding for an about 56 kDa polypeptide, a recombinant expression vector containing the DNA fragment, the 56 kDa polypeptide and a monoclonal antibody reactive with the peptide, and a method of assaying for antibodies reactive with the 56 kDa peptide.

=> d l2 3 kwic

L2 ANSWER 3 OF 8 USPATFULL
DETD . . . mismatch, even a single mismatch within a probe that is 20-30 nucleotides long. A mismatch has a disruptive effect on

hybridization which make perfectly matching **probes** thermodynamically favored over **mismatched probes**. For example, a mismatched **probe** will have a lower **melting temperature** (T.sub.m) than a perfectly matched **probe**. Multiple **mismatches** have an even greater disruptive effect on **hybridization** than single mismatches. As a result, multiple mismatch **probes** are even less thermodynamically favored than perfectly matched probes.

=> d l2 5 kwic

L2 ANSWER 5 OF 8 USPATFULL
DETD . . . mismatch, even a single mismatch within a probe that is 20-30 nucleotides long. A mismatch has a disruptive effect on **hybridization** which make perfectly matching **probes** thermodynamically favored over **mismatched probes**. For example, a mismatched **probe** will have a lower **melting temperature** (T.sub.m) than a perfectly matched **probe**. Multiple **mismatches** have an even greater disruptive effect on **hybridization** than single mismatches. As a result, multiple mismatch **probes** are even less thermodynamically favored than perfectly matched probes.

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